

sequences, SEQ ID NOs:1-38, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.

This amendment contains no new matter. The amendments to the specification and claims introducing sequence ID numbers simply provide appropriate cross-reference from the sequences in the application to the formal sequence listing. Replacement Figures 5 and 6 also introduce no new matter. The letters that are now visible in the "POINTED/A-REGION" and the "ETS-DNA Binding Domain" can be determined by reference to Figure 4 and to SEQ ID NO 15 as filed. The corrections to the mESX sequence in Figures 5 and 6 can be determined by reference to the mESX sequence in the Sequence Listing as filed. Moreover, it is noted that the specification teaches that Applicants isolated and sequenced the human and mouse ESX genes. The corrections to Figures 5 and 6 simply reflect the correct polypeptide sequence and as such, are inherent in the isolated nucleic acids (*see, e.g., Kennecott Corp. v Kyocera Internat., Inc. and Kyoto Ceramic Co., Ltd.* 5 USPQ2d 1194 (Fed. Cir. 1987))

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at (415) 576-0200.

Respectfully submitted,



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ESX Primary Structure and Domain Homologies.

mESX 1 MAATCEISNVFSNYFSNAMYSSDPTLAPAPP.TTFGTEDLVLT LNNQOMT 49
|||||:||||| ||| ||| :||||| |||
hESX 1 MAATCEISNIFSNYFSAMYSSDSTLASVPPAATFGADDLVLT LSNPQMS 50

E_2/E_3
↓

mESX 50 LEGPEKASWTSERPQFWSKTQVLEWISYQVEKNKYDASSIDFSRCNMDGA 99
||| ||| :||||| ||| ||| :||||| |||
hESX 51 LEGTEKASWLGEQPQFWSKTQVLDWISYQVEKNKYDASAIIDFSRCDMDGA 100

E_3/E_4
↓

mESX 100 TLCSCALEELRLVFGPLGDQLHAQLRDLTSNSSDEL SWIIELLEKDGMSF 149
||| . ||||| :||||| ||| ||| :||||| |||
hESX 101 TLCNCALEELRLVFGPLGDQLHAQLRDLTSSSSDEL SWIIELLEKDGMAF 150

E_1/E_5 ↓ E_5/E_6 ↓

mESX 150 QESLGLDLPSTDQGSPPFAQELLDDGRQASPYCYCSTYGP GAPSPGSSDVSTA 199
||| . ||||| :||||| ||| ||| :||||| |||
hESX 151 QEAL.DPGPFDQGSPPFAQELLDDGQQASPYHPGSCGAGAPSPGSSDVSTA 199

E_6/E_7 ↓

mESX 200 **R** STATPQSSHASDSGGSDVDLDLTESKVFPRDDFTDYKKGEPKHGKRKRGR 249
||| . ||||| :||||| ||| ||| :||||| |||
hESX 200 GTGASRSSHSSDSGGSDVDLDPTDGKLFPSDGRDCKKGD PKHGKRKRGR 249

E_7/E_8
↓

mESX 250 PRKLSKEYWDCLEGKSKHAPRGTE **POINTED / A-Region** 299
||| ||| :||||| ||| ||| :||||| |||
hESX 250 PRKLSKEYWDCLEGKSKHAPRGTE **Serine-Rich Box** 299

E_8/E_9
↓

mESX 300 **Nuclear Targeting Sequences** 349
||| ||| :||||| ||| ||| :||||| |||
hESX 300 **Nuclear Targeting Sequences** 349

mESX 350 **POINTED / A-Region** GKNSSGWKEEEVGESRN 371
||| ||| :||||| ||| ||| :||||| |||
hESX 350 **Serine-Rich Box** GKNSSGWKEEEVLQSRN 371

— POINTED / A-Region
■ Serine-Rich Box
Nuclear Targeting Sequences

Fig. 5

mESX -347 TCAGCCCTGGCCAGGCCCCCCAGGAAGAATTTCACGCGCCAGAGGGCAGCC -298
|| ||| | | | | | | | | | | | | | | | |
hESX -350 CCATCTCTGGCCTGGCCCCCTGGGAGGAATTTCCTGGGCCAGAGGGCAGCC -301

mESX -297 TAAGGCACAGATGCCCAACCCTGCAATGTTCCTGCCACCTGCCAGTTCA -246
|| ||| | | | | | | | | | | | | | | | |
hESX -300 GAAAGCACAGATGCCCAACCCTGCAACGTTCCTGCCACCTGCCAGGCCA -251

mESX -247 GTACCCAGGGCCCAACCCCAGAGGGTGCGGAATGACAGATTCTGACAATC -198
|| ||| | | | | | | | | | | | | | | | |
hESX -250 GTGCCCCGTGCCCAACCCCAGAGGGTGCGGGATGACAGACTCTGACAATC -201

mESX -197 ATTAAACCAGCCAGGCCTGATTTCCAGCACCGCCTGCTAGGATCTGGGC -146
|| ||| | | | | | | | | | | | | | | | |
hESX -200 ATTAAACCAGCCGGGCCTGATTTCCAGCACTGCCTGCTAAGATCCGGGC -151

mESX -147 CAAGTGGCACGGAATATGCAAATCACCTGGGACAGGGAGCCCAGTCTGAA -98
|| ||| | | | | | | | | | | | | | | | |
hESX -150 CAAGTGGCACTGAATATGCAAATCACCTGGGGCCAGGAGCCCAGTCTAAA -101

mESX -97 GGCCAGGAAATCCCCAGCATCCAATGAGCCACCAGCTCAGGTTACAACCG -46
|| ||| | | | | | | | | | | | | | | | |
hESX -100 GGCCAGGAAATCCCCTCCATCCAATGAGACACCAGCTCAGGTTACTGCAG -49

mESX -47 GGGACGTACGCCGAAGACCTG...GAGGGGAGGAGCTCCTGCTTTGCTCT -1
|||| | | | | | | | | | | | | | | |
hESX -50 GGGACACACTATAAAGCCCTGAGCTCAGGGAGGAGCTCCCTCCAGGCTCT -1

mESX +1 ATTTAGAGCGGGTGGGGGCAGCGCCCTGGCCCACTCATCACTGCTACCT +50
||||| | | | | | | | | | | | | | | |
hESX +1 ATTTAGAGCGGGTAGGGGAGCGCAGCGCCAGATACCTCAGCGCTACCT +50

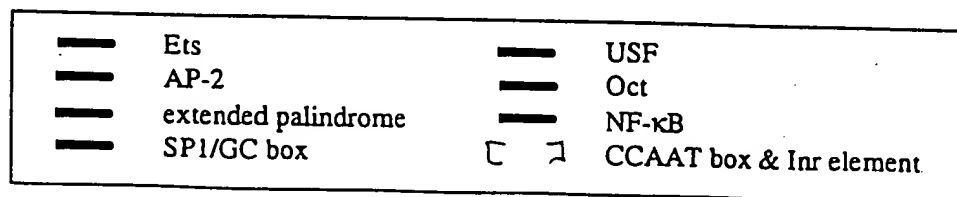


Fig. 6